

#19



RAW SEQUENCE LISTING

DATE: 11/04/2002

PATENT APPLICATION: US/09/478,598

TIME: 16:19:28

Input Set : N:\Crf3\RULE60\09478598.raw

Output Set: N:\CRF4\11042002\I478598.raw

1 <110> APPLICANT: Rao, Gururaj A.
 2 Major Sleister, Heidi
 3 <120> TITLE OF INVENTION: Compositions and Methods for Altering Amino Acid
 4 Content of Proteins
 5 <130> FILE REFERENCE: 5718-16
 6 <140> CURRENT APPLICATION NUMBER: 09/478,598
 7 <141> CURRENT FILING DATE: 2000-01-06
 9 <150> PRIOR APPLICATION NUMBER: US/08/988,015
 10 <151> PRIOR FILING DATE: 1997-12-10
 12 <160> NUMBER OF SEQ ID NOS: 11
 13 <170> SOFTWARE: PatentIn Ver. 2.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 218
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Glycine max
 19 <400> SEQUENCE: 1

20	Arg	Ser	Ser	Glu	Val	Lys	Cys	Ala	Ser	Phe	Arg	Leu	Ala	Val	Glu	Ala
21	1				5					10					15	
22	His	Asn	Ile	Arg	Ala	Phe	Lys	Thr	Ile	Pro	Glu	Glu	Cys	Val	Ser	Pro
23				20					25					30		
24	Thr	Lys	Asp	Tyr	Ile	Asn	Gly	Glu	Gln	Phe	Arg	Ser	Asp	Ser	Lys	Thr
25			35					40					45			
26	Val	Asn	Gln	Gln	Ala	Phe	Phe	Tyr	Ala	Ser	Glu	Arg	Glu	Val	His	His
27		50					55				60					
28	Asn	Asp	Ile	Phe	Ile	Phe	Gly	Ile	Asp	Asn	Thr	Val	Leu	Ser	Asn	Ile
29	65					70				75				80		
30	Pro	Tyr	Tyr	Glu	Lys	His	Gly	Tyr	Gly	Val	Glu	Glu	Phe	Asn	Glu	Thr
31				85						90				95		
32	Leu	Tyr	Asp	Glu	Trp	Val	Asn	Lys	Gly	Asp	Ala	Pro	Ala	Leu	Pro	Glu
33			100						105					110		
34	Thr	Leu	Lys	Asn	Tyr	Asn	Lys	Leu	Leu	Ser	Leu	Gly	Phe	Lys	Ile	Val
35			115					120					125			
36	Phe	Leu	Ser	Gly	Arg	Tyr	Leu	Asp	Lys	Met	Ala	Val	Thr	Glu	Ala	Asn
37		130					135					140				
38	Leu	Lys	Lys	Ala	Gly	Phe	His	Thr	Trp	Glu	Gln	Leu	Ile	Leu	Lys	Asp
39	145					150				155				160		
40	Pro	His	Leu	Ile	Thr	Pro	Asn	Ala	Leu	Ser	Tyr	Lys	Ser	Ala	Met	Arg
41				165					170					175		
42	Glu	Asn	Leu	Leu	Arg	Gln	Gly	Tyr	Arg	Ile	Val	Gly	Ile	Ile	Gly	Asp
43				180					185				190			
44	Gln	Trp	Ser	Asp	Leu	Leu	Gly	Asp	His	Arg	Gly	Glu	Ser	Arg	Thr	Phe
45			195				200						205			
46	Lys	Leu	Pro	Asn	Pro	Met	Tyr	Ile	Glu							

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50 <211> LENGTH: 218
51 <212> TYPE: PRT
52 <213> ORGANISM: Glycine max
53 <400> SEQUENCE: 2
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56   His Asn Ile Phe Gly Phe Glu Thr Ile Pro Glu Glu Cys Val Glu Ala
57             20              25              30
58   Thr Lys Glu Tyr Ile His Gly Glu Gln Tyr Arg Ser Asp Ser Lys Thr
59             35              40              45
60   Val Asn Gln Gln Ala Tyr Phe Tyr Ala Arg Asp Leu Glu Val His Pro
61             50              55              60
62   Lys Asp Thr Phe Val Phe Ser Ile Asp Asn Thr Val Leu Ser Asn Ile
63             65              70              75              80
64   Pro Tyr Tyr Lys Lys His Gly Tyr Gly Val Glu Lys Phe Asn Ser Thr
65             85              90              95
66   Leu Tyr Asp Glu Trp Val Asn Lys Gly Asn Ala Pro Ser Leu Pro Glu
67             100             105             110
68   Thr Leu Lys Asn Tyr Asn Lys Leu Val Ser Leu Gly Phe Lys Ile Ile
69             115             120             125
70   Phe Leu Ser Gly Arg Thr Leu Asp Lys Gln Ala Val Thr Glu Ala Asn
71             130             135             140
72   Leu Lys Lys Ala Gly Tyr His Thr Trp Glu Lys Leu Ile Leu Lys Asp
73             145             150             155             160
74   Pro Gln Pro Ser Thr Pro Asn Ala Val Ser Tyr Lys Thr Ala Ala Arg
75             165             170             175
76   Glu Lys Leu Ile Arg Gln Gly Tyr Asn Ile Val Gly Ile Ile Gly Asp
77             180             185             190
78   Gln Trp Ser Asp Leu Leu Gly Gly His Arg Gly Glu Ser Arg Thr Phe
79             195             200             205
80   Lys Leu Pro Asn Pro Leu Tyr Tyr Ile Gln
81     210          215
82
83 <210> SEQ ID NO: 3
84 <211> LENGTH: 214
85 <212> TYPE: PRT
86 <213> ORGANISM: Lycopersicon esculentum
87 <400> SEQUENCE: 3
88   Leu Lys Cys Thr Thr Trp Arg Phe Val Val Glu Thr Asn Asn Leu Ser
89     1              5              10              15
90   Pro Trp Lys Thr Ile Pro Glu Glu Cys Ala Asp Tyr Val Lys Glu Tyr
91             20              25              30
92   Met Val Gly Pro Gly Tyr Lys Met Glu Ile Asp Arg Val Ser Asp Glu
93             35              40              45
94   Ala Gly Glu Tyr Ala Lys Ser Val Asp Leu Gly Asp Asp Gly Arg Asp
95             50              55              60
96   Val Trp Ile Phe Asp Val Asp Glu Thr Leu Leu Ser Asn Leu Pro Tyr
97             65              70              75              80

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98      Tyr Ser Asp His Arg Tyr Gly Leu Glu Val Phe Asp Asp Val Glu Phe
99              85              90              95
100     Asp Lys Trp Val Glu Asn Gly Thr Ala Pro Ala Leu Gly Ser Ser Leu
101              100              105              110
102     Lys Leu Tyr Gln Glu Val Leu Lys Leu Gly Phe Lys Val Phe Leu Leu
103              115              120              125
104     Thr Gly Arg Ser Glu Arg His Arg Ser Val Thr Val Glu Asn Leu Met
105              130              135              140
106     Asn Ala Gly Phe His Asp Trp His Lys Leu Ile Leu Arg Gly Ser Asp
107     145              150              155              160
108     His Gly Lys Thr Ala Thr Thr Tyr Lys Ser Glu Arg Arg Asn Ala Met
109              165              170              175
110     Val Glu Glu Gly Phe Arg Ile Val Gly Asn Ser Gly Asp Gln Trp Ser
111              180              185              190
112     Asp Leu Leu Gly Ser Ser Met Ser Tyr Arg Ser Phe Lys Leu Pro Asn
113              195              200              205
114     Pro Met Tyr Tyr Ile Leu
115              210
117 <210> SEQ ID NO: 4
118 <211> LENGTH: 217
119 <212> TYPE: PRT
120 <213> ORGANISM: Phaseolus vulgaris
121 <400> SEQUENCE: 4
122     Ser Asp Thr Glu Val Arg Cys Ala Ser Trp Arg Leu Ala Val Glu Ala
123     1              5              10              15
124     Gln Asn Ile Phe Gly Phe Glu Thr Ile Pro Gln Gln Cys Val Asp Ala
125              20              25              30
126     Thr Ala Asn Tyr Ile Glu Gly Gly Gln Tyr Arg Ser Asp Ser Lys Thr
127              35              40              45
128     Val Asn Gln Gln Ile Tyr Phe Phe Ala Arg Asp Arg His Val His Glu
129              50              55              60
130     Asn Asp Val Ile Leu Phe Asn Ile Asp Gly Thr Ala Leu Ser Asn Ile
131              65              70              75              80
132     Pro Tyr Tyr Ser Gln His Gly Tyr Gly Ser Glu Lys Phe Asp Ser Glu
133              85              90              95
134     Arg Tyr Asp Glu Glu Phe Val Asn Lys Gly Glu Ala Pro Ala Leu Pro
135              100              105              110
136     Glu Thr Leu Lys Asn Tyr Asn Lys Leu Val Ser Leu Gly Tyr Lys Ile
137              115              120              125
138     Ile Phe Leu Ser Gly Arg Leu Lys Asp Lys Arg Ala Val Thr Glu Ala
139              130              135              140
140     Asn Leu Lys Lys Ala Gly Tyr Asn Thr Trp Glu Lys Leu Ile Leu Lys
141     145              150              155              160
142     Asp Pro Ser Asn Ser Ala Glu Asn Val Val Tyr Lys Thr Ala Glu Arg
143              165              170              175
144     Ala Lys Leu Val Gln Glu Gly Tyr Arg Ile Val Gly Asn Ile Gly Asp
145              180              185              190
146     Gln Trp Asn Asp Leu Lys Gly Glu Asn Arg Ala Ile Arg Ser Phe Lys
147              195              200              205

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148      Leu Pro Asn Pro Met Tyr Tyr Thr Lys
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151 <210> SEQ ID NO: 5
152 <211> LENGTH: 214
153 <212> TYPE: PRT
154 <213> ORGANISM: Arabidopsis thaliana
155 <400> SEQUENCE: 5
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157          1                5                10                15
158      Asn Phe Asp Thr Val Pro Ala Asn Cys Lys Ala Tyr Val Glu Asp Tyr
159          20                25                30
160      Leu Ile Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys Thr Val Asn Lys
161          35                40                45
162      Glu Ala Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys Asn Asp Thr Ile
163          50                55                60
164      Asn Val Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu Ser Ser Ile Pro
165          65                70                75                80
166      Tyr Tyr Ala Lys Tyr Gly Tyr Gly Thr Glu Asn Thr Ala Ala Gly Ala
167          85                90                95
168      Tyr Trp Ser Trp Leu Val Ser Gly Glu Thr Pro Gly Leu Pro Glu Thr
169          100               105               110
170      Leu His Leu Tyr Glu Asn Leu Leu Glu Leu Gly Ile Glu Pro Ile Ile
171          115               120               125
172      Ile Ser Asp Arg Trp Lys Lys Leu Ser Glu Ile Thr Ile Glu Asn Leu
173          130               135               140
174      Lys Ala Val Gly Val Thr Lys Trp Lys His Val Ile Leu Lys Pro Asn
175          145               150               155               160
176      Gly Lys Leu Thr Gln Val Val Tyr Lys Ser Lys Val Arg Asn Gly Leu
177          165               170               175
178      Val Arg Gln Gly Tyr Asn Ile Val Gly Ile Ile Gly Asp Gln Trp Ala
179          180               185               190
180      Asp Leu Val Glu Asp Thr Pro Gly Arg Val Phe Lys Leu Pro Asn Pro
181          195               200               205
182      Leu Tyr Tyr Val Pro Ser
183          210
185 <210> SEQ ID NO: 6
186 <211> LENGTH: 220
187 <212> TYPE: PRT
188 <213> ORGANISM: Arabidopsis thaliana
189 <400> SEQUENCE: 6
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191          1                5                10                15
192      Ser Asn Ile Ile Asn Phe Asp Thr Val Pro Ala Asn Cys Lys Ala Tyr
193          20                25                30
194      Val Glu Asp Tyr Leu Ile Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys
195          35                40                45
196      Thr Val Asn Lys Glu Ala Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys
197          50                55                60
198      Asn Asp Thr Val Asn Val Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu

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199      65      70      75      80
200  Ser Ser Ile Pro Tyr Tyr Ala Lys Tyr Gly Tyr Gly Thr Glu Asn Thr
201      85      90      95
202  Ala Pro Gly Ala Tyr Trp Ser Trp Leu Glu Ser Gly Glu Ser Thr Pro
203      100      105      110
204  Gly Leu Pro Glu Thr Leu Tyr Leu Tyr Glu Asn Leu Leu Glu Leu Gly
205      115      120      125
206  Ile Glu Pro Ile Ile Ile Ser Asp Arg Trp Lys Lys Leu Ser Glu Val
207      130      135      140
208  Thr Val Glu Asn Leu Lys Ala Val Gly Val Thr Lys Trp Lys His Leu
209      145      150      155      160
210  Ile Leu Lys Pro Asn Gly Ser Lys Leu Thr Gln Val Val Tyr Lys Ser
211      165      170      175
212  Lys Val Arg Asn Ser Leu Val Lys Lys Gly Tyr Asn Ile Val Gly Asn
213      180      185      190
214  Ile Gly Asp Gln Trp Ala Asp Leu Val Glu Asp Thr Pro Gly Arg Val
215      195      200      205
216  Phe Lys Leu Pro Asn Pro Leu Tyr Tyr Val Pro Ser
217      210      215      220
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220 <211> LENGTH: 219
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225      1      5      10      15
226  Ser Asn Ile Ile Asp Phe Asp Thr Val Pro Ala Asn Cys Lys Asp Tyr
227      20      25      30
228  Val Glu Asp Tyr Leu Ile Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys
229      35      40      45
230  Thr Val Cys Lys Glu Ala Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys
231      50      55      60
232  Asn Asp Thr Val Asn Val Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu
233      65      70      75      80
234  Ser Ser Ile Pro Tyr Tyr Ala Lys Tyr Gly Tyr Gly Thr Glu Lys Thr
235      85      90      95
236  Asp Pro Gly Ala Tyr Trp Leu Trp Leu Gly Thr Gly Ala Ser Thr Pro
237      100      105      110
238  Gly Leu Pro Glu Gly Leu Tyr Leu Tyr Gln Asn Ile Ile Glu Val Gly
239      115      120      125
240  Ile Glu Pro Ile Ile Leu Ser Val Arg Trp Lys Leu Trp Lys Asn Val
241      130      135      140
242  Thr Leu Asn Leu Glu Ala Ala Gly Val Thr Tyr Trp Lys His Leu Ile
243      145      150      155      160
244  Leu Lys Pro Asn Gly Ser Asn Leu Arg Gln Val Val Tyr Lys Ser Lys
245      165      170      175
246  Val Arg Asn Lys Leu Val Lys Lys Gly Tyr Asn Ile Val Gly Asn Ile
247      180      185      190
248  Gly Asp Gln Trp Ala Asp Leu Val Glu Asp Thr Pro Gly Arg Val Phe

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VERIFICATION SUMMARY

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